



Summary of Blood Typing Work during 7 Years (1955-1962)  
by Wilmer J. Miller

Serology Laboratory, University of California at Davis  
for the  
Purebred Dairy Cattle Association  
(Ayrshire, Brown Swiss, Guernsey, Jersey and Holstein-Friesian)

Table 1. Number of samples, percentage cases and solutions.

Cases	Total
Number of samples tested	12,192
Number of percentage cases	1,259
Number of percentage cases solved	1,129
Percent of percentage cases solved	90 %
Number of spot checks	859
Number of exclusions in spot checks	60
Percent of exclusions in spot checks	7 %

\* Omitting 28 special herd problems.  
\*\* 51 of the 130 cases not solved involved cases in which one parent was not available or bulls types elsewhere were involved. Omitting these 51 cases, the percent solved would be 1129/1208 = 93.5%

Table 2. Frequency of blood group systems critically involved in solving percentage problems

Cases	B	C	F	A	S	Z	L	J	H
1,259 (*)	74%	27%	12%	12%	11%	10%	7%	6%	3%

\* Approximately 90% Holstein-Friesian.

Average number of systems critically involved per case = 1.6%.  
103/1259 = 8% of the cases that were not possible to solve by factor analysis were solved by phenogrouping.

With increased use of artificial insemination in cattle in the 1950's, cases multiplied in which semen from 2 or more bulls was used to "settle" (induce pregnancy in) a cow. Blood typing became the major tool for excluding or "qualifying" parents and was used frequently. Phenogroups in one system are separated by a slash, and dash ("-") indicates the absence of any detected factor (open system).

Table 3. Examples of Percentage Problems in Cattle

Sample	Blood Group Systems									
	A	B	C	F	J	L	M	S	Z	
Sample 1	DH	RO <sub>2</sub> Y <sub>1</sub> A'E <sub>1</sub> G <sub>1</sub> /I <sub>2</sub> Z <sub>2</sub> E <sub>1</sub> Y <sub>1</sub>	C <sub>1</sub> X <sub>1</sub> /EW	F/F	-/-	-/-	-/-	H'	Z/Z	
Bull 1	D/D	RO <sub>1</sub> /D'E <sub>1</sub> F <sub>1</sub> G <sub>1</sub> O <sub>1</sub>	C <sub>2</sub> EW/	F/V	J	L	-/-	SH'/Z/-		
Bull 2	D/D	RO <sub>1</sub> /D'E <sub>1</sub> F <sub>1</sub> G <sub>1</sub> O <sub>1</sub>	C <sub>2</sub> EW/	F/V	J	L	-/-	SH'/Z/-		
Calf	A/D	RO <sub>1</sub> /OY <sub>1</sub> E <sub>1</sub>	E	F/F	J	L	-/-	H'	Z/-	
Calf	D/D	OY <sub>2</sub> E <sub>1</sub> /D'E <sub>1</sub> F <sub>1</sub> G <sub>1</sub> O <sub>1</sub>	C <sub>2</sub> EW/	F/V	J	L	-/-	SH'/-/-		

Solution: The calf possesses phenogroups D, D'E<sub>1</sub>F<sub>1</sub>G<sub>1</sub>O<sub>1</sub>, C<sub>2</sub>EW, V, SH', and dash in the Z system which must have been transmitted by the sire if the dam 1 is the true dam. Bull 1 lacks D'E<sub>1</sub>F<sub>1</sub>G<sub>1</sub>O<sub>1</sub>, V, SH' and dash in the Z system and, therefore, is excluded as the sire. Further, neither of Bull 1's B phenogroups appear in the calf also excluding him as the sire by any dam. Bull 2 possesses the critical phenogroups and qualifies as the sire.

Sample 2. Holstein-Friesian: Dam unavailable. Shows superiority of phenogrouping over factor analysis.

Bull 1	D/D	Y <sub>1</sub> E <sub>1</sub> G <sub>1</sub> Y <sub>1</sub> /Y <sub>2</sub> A <sub>1</sub>	X <sub>2</sub>	F/F	J	L	-/-	H'	Z/-
Bull 2	A/D	O <sub>1</sub> A/D'E <sub>1</sub> F <sub>1</sub> G <sub>1</sub> O <sub>1</sub>	C <sub>1</sub> E/C <sub>1</sub> /X <sub>1</sub>	F/F	-/-	-/-	-/-	H'	-/-
Calf	A/D	O <sub>1</sub> A/FI <sub>1</sub>	C <sub>1</sub> E/	F/F	J	-/-	-/-	H'	-/-

Solution: The calf possesses two B system phenogroups both missing in Bull 1 including him as the sire by any dam. Moreover, neither of his B groups appear in the calf also excluding him as the sire by any dam. Bull 2 possesses the B group in common with the calf and otherwise qualifies as the sire (by a dam possessing F<sub>1</sub>, F and J).

Sample 3. Holstein-Friesian. Rare case (about 6% in 1962).

Bull 1	A/D	RO <sub>2</sub> Y <sub>1</sub> A'E <sub>1</sub> G <sub>1</sub> /	X <sub>2</sub>	F/F	-/-	-/-	-/-	H'	-/-
Bull 2	A <sub>1</sub> (DH)	RO <sub>2</sub> Y <sub>1</sub> A'E <sub>1</sub> G <sub>1</sub> /B <sub>2</sub> GO <sub>1</sub>	C <sub>1</sub> E/X <sub>2</sub>	F/F	-/-	-/-	-/-	H'	-/-
Bull 1	D/D	I <sub>2</sub> /E <sub>1</sub>	C <sub>1</sub> X <sub>1</sub> /X <sub>2</sub> L	F/F	-/-	-/-	-/-	SH'/Z/-	
Calf	D/D	RO <sub>2</sub> Y <sub>1</sub> A'E <sub>1</sub> G <sub>1</sub> /I <sub>2</sub>	C <sub>1</sub> X <sub>1</sub> /	F/F	-/-	-/-	-/-	SH'/-/-	

Solution: The calf possesses D, RO<sub>2</sub>Y<sub>1</sub>A'E<sub>1</sub>G<sub>1</sub>, and F transmitted by the sire if Dam 1 is the true dam. Both bull 1 and bull 2 possesses the critical groups and qualify as the sire. NO solution. This is where additional systems are helpful.

Summary of Blood Typing Work during 7 Years (1955-1962)  
by Wilmer J. Miller

Serology Laboratory, University of California at Davis  
for the  
Furebred Dairy Cattle Association  
(Ayrshire, Brown Swiss, Guernsey, Jersey and Holstein-Friesian)

Table 1. Number of samples, parentage cases and solutions.

Cases	Total
Number of samples tested	12,192
Number of parentage cases	1,259
Number of parentage cases solved	1,129
Percent of parentage cases solved	90%
Number of spot checks	859
Number of exclusions in spot checks	60
Percent of exclusions in spot checks	7%

\* Omitting 28 special herd problems.  
\*\* 51 of the 130 cases not solved involved cases in which one parent was not available or bulls types elsewhere were involved. Omitting these 51 cases, the percent solved would be 1129/1208 = 93.5%.

Table 2. Frequency of blood group systems critically involved in solving parentage problems

Cases	B	C	F	A	S	Z	L	J	M
1,259(*)	74%	27%	12%	12%	11%	10%	7%	6%	3%

\* Approximately 90% Holstein-Friesian.  
Average number of systems critically involved per case = 1.6%.  
103/1259 = 8% of the cases that were not possible to solve by factor analysis were solved by phenogrouping.

With increased use of artificial insemination in cattle in the 1950's, cases multiplied in which semen from 2 or more bulls was used to "settle" (induce pregnancy in) a cow. Blood typing became the major tool for excluding or "qualifying" parents and was used frequently. Phenogroups in one system are separated by a slash, and dash ("-") indicates the absence of any detected factor (open system).

Table 3. Examples of Parentage Problems in Cattle

Sample	Blood Group Systems									
	A	B	C	F	J	L	M	S	Z	Z
Bull 1	DH	R <sub>0</sub> Y <sub>1</sub> A'E <sub>1</sub> G <sub>1</sub> I <sub>2</sub> Z <sub>1</sub> E <sub>1</sub> Y <sub>1</sub>	C <sub>1</sub> X <sub>1</sub> /EW	F/F	-/-	-/-	-/-	H'	Z/Z	
Bull 2	D/D	R <sub>0</sub> 1/D'E <sub>1</sub> F <sub>1</sub> G <sub>1</sub> O <sub>1</sub>	C <sub>2</sub> EW/	F/V	J	L	-/-	SH'/Z/-		
Bull 1	A <sub>1</sub> /D	R <sub>0</sub> 1/GY <sub>1</sub> E <sub>1</sub>	E	F/F	J/J	L	-/-	H'/Z/-		
Bull 1	D/D	GY <sub>1</sub> E <sub>1</sub> /D'E <sub>1</sub> F <sub>1</sub> G <sub>1</sub> O <sub>1</sub>	C <sub>2</sub> EW/	F/V	J	L	-/-	SH'/-/-		

Solution: The calf possesses phenogroups D, D'E<sub>1</sub>F<sub>1</sub>G<sub>1</sub>O<sub>1</sub>, C<sub>2</sub>EW, V, SH', and dash in the Z system which must have been transmitted by the sire if the dam 1 is the one dam. Bull 1 one lacks D'E<sub>1</sub>F<sub>1</sub>G<sub>1</sub>O<sub>1</sub>, V, SH' and dash in the Z system and, therefore, is excluded as the sire. Further, neither of Bull 1's B phenogroups appear in the calf also excluding him as the sire by any dam. Bull 2 possesses the critical phenogroups and qualifies as the sire.

Table 2. Holstein-Friesian; Dam unavailable. Shows superiority of phenogrouping over factor analysis.

Bull 1	D/D	Y <sub>1</sub> E <sub>1</sub> G <sub>1</sub> Y <sub>1</sub> Z <sub>1</sub> A <sub>1</sub>	X <sub>2</sub>	F/F	J	L	-/-	H'	Z/-
Bull 2	A <sub>1</sub> /D	Q <sub>1</sub> A <sub>1</sub> /D'E <sub>1</sub> F <sub>1</sub> G <sub>1</sub> O <sub>1</sub>	C <sub>1</sub> E/C <sub>1</sub> X <sub>1</sub>	F/F	-/-	-/-	-/-	H'	-/-
Bull 1	A <sub>1</sub> /D	Q <sub>1</sub> A <sub>1</sub> /F <sub>1</sub> I <sub>1</sub>	C <sub>1</sub> E/	F/F	J	-/-	-/-	H'	-/-

Solution: The calf possesses two B system phenogroups both missing in Bull 1 including him as the sire by any dam. Moreover, neither of his B groups appear in the calf also excluding him as the sire by any dam. Bull 2 possesses the B group in common with the calf and otherwise qualifies as the sire (by a dam possessing F<sub>1</sub>, F and J).

Table 3. Holstein-Friesian, rare case (about 6% in 1962).

Bull 1	A <sub>1</sub> /D	R <sub>0</sub> Y <sub>1</sub> A'E <sub>1</sub> G <sub>1</sub> /	X <sub>2</sub>	F/F	-/-	-/-	-/-	H'	-/-
Bull 2	A <sub>1</sub> (D)H	R <sub>0</sub> Y <sub>1</sub> A'E <sub>1</sub> G <sub>1</sub> /R <sub>2</sub> G <sub>1</sub>	C <sub>1</sub> E/X <sub>2</sub>	F/F	-/-	-/-	-/-	H'	-/-
Bull 1	D/D	I <sub>2</sub> /E <sub>1</sub>	C <sub>1</sub> X <sub>1</sub> /X <sub>2</sub> L	F/F	-/-	-/-	-/-	SH'/Z/-	
Bull 1	D/D	R <sub>0</sub> Y <sub>1</sub> A'E <sub>1</sub> G <sub>1</sub> /I <sub>2</sub>	C <sub>1</sub> X <sub>1</sub> /	F/F	-/-	-/-	-/-	SH'/-/-	

Solution: The calf possesses D, R<sub>0</sub>Y<sub>1</sub>A'E<sub>1</sub>G<sub>1</sub>, and F transmitted by the sire if the dam 1 is the true dam. Both bull 1 and bull 2 possess the critical groups and qualify as the sire. NO solution. This is where additional systems are helpful.

Example 4. Arysthrie. Note the utility of phenogrouping.

Bull 1	A <sub>2</sub> D/	-/-	X <sub>2</sub>	F/F	-/-	-/-	-/-	H <sub>1</sub>
Bull 2	A <sub>1</sub> (D)	0 <sub>1</sub> A <sub>1</sub> 'Y <sub>1</sub> E <sub>1</sub> 'S <sub>1</sub> G <sub>1</sub> 'Y <sub>1</sub>	C <sub>1</sub> EX <sub>2</sub>	F/F	-/-	-/-	-/-	H <sub>1</sub>
Bull 3	A <sub>1</sub> (D)H	BGX <sub>2</sub> E <sub>2</sub> 'F <sub>2</sub> 'O <sub>1</sub> I <sub>1</sub> E <sub>1</sub> 'S <sub>1</sub> F <sub>1</sub> 'K <sub>1</sub>	C <sub>1</sub> EWX <sub>2</sub>	F/V	±0	-/-	-/-	H <sub>1</sub>
Dam 1	A <sub>1</sub> D	0 <sub>1</sub> A <sub>1</sub> 'E <sub>1</sub> 'S <sub>1</sub> G <sub>1</sub> 'Y <sub>1</sub>	C <sub>1</sub> EX <sub>2</sub>	F/F	0	L	-/-	H <sub>1</sub>
Calf	A <sub>1</sub> D	B0 <sub>1</sub> Y <sub>2</sub> D <sub>1</sub> '/60	X <sub>2</sub>	F/V	-/-	L	-/-	H <sub>1</sub>

Solution: The calf possesses the B system phenogroups B0<sub>1</sub>Y<sub>2</sub>D<sub>1</sub> and G0<sub>1</sub> neither which appear in any of the putative parents including Dam 1. Therefore, all are excluded as parent. (Also note the absence of S in any of the putative parents.) Further analysis would allow bull 3 to qualify by dam 1.

Example 5. Guernsey. Are the calves Lottie and Louise Twins? Which bull is the sire?

Bull 1	A <sub>1</sub> DH	IE <sub>1</sub> '/I <sub>1</sub> '	X <sub>2</sub>	F/F	-/-	-/-	-/-	SH <sub>1</sub> '
Bull 2	A <sub>1</sub> (D)	0 <sub>1</sub> I <sub>1</sub> '/0 <sub>1</sub>	EW	F/F	0	-/-	-/-	SH <sub>1</sub> '
Dam 1	D/D	B1/60 <sub>1</sub> 0	C <sub>1</sub> ER <sub>2</sub> X <sub>2</sub>	F/F	(0)	-/-	-/-	H <sub>1</sub>
Lottie	A <sub>1</sub> DH	±B1I <sub>1</sub> '±G±0 <sub>1</sub> ±B0±I <sub>1</sub> '/±IE <sub>1</sub> ' <sub>1</sub>	(±W)X <sub>2</sub>	F/F	-/-	-/-	-/-	±SH <sub>1</sub> '/±I <sub>1</sub>
Louise	A <sub>1</sub> DH	±B1I <sub>1</sub> '±G±0 <sub>1</sub> ±B0±I <sub>1</sub> '/±IE <sub>1</sub> ' <sub>1</sub>	(±W)X <sub>2</sub>	F/F	-/-	-/-	-/-	±SH <sub>1</sub> '/±I <sub>1</sub>

± signifies an atypically weak reaction

Solution: Since Lottie and Louise possess identical blood types, they are twin interchanges of early migratory red cell progenitors). The twins possess groups and H<sub>1</sub>I<sub>1</sub>' and IE<sub>1</sub>'/W, F, and SH which must have been transmitted by the sire. The dam 1 is the true dam. (Note that the I<sub>1</sub>' of the twins may have phenogroup 0<sub>1</sub>I<sub>1</sub>' since the G0<sub>1</sub> phenogroup covers 0<sub>1</sub>). Bull 1 lacks W and so cannot be the sire of both twins. Bull 2 lacks H<sub>1</sub> and IE<sub>1</sub>' and so cannot be the sire of both twins. Together the bulls possess the critical groups, so one is the sire of one twin and the other the sire of the other twin. Which is the sire of which twin cannot be decided with only this information. When the twins have offspring, their genetic contribution from a particular sire should be evident.

Since these 1962 examples the number of phenogroups has doubled and the additional systems R<sub>1</sub> and T<sub>1</sub> added. Further, the of electrophoretic systems detecting polymorphism of hemoglobin transferrin, albumin, and carbonic anhydrase systems have been added although they cost considerably more and are seldom needed to answer most questions. Restriction endonuclease patterns may be adapted to degrees of heterozygosity leading to HA as well as solving parental problems. But again the expense is considerable. We can confine our attentions to just the red cell systems.

In spite of all these complexities the analysis of the blood typing results is reasonably straightforward. All blood typing analyses for parentage include factor analysis. If the offspring has a particular factor, then one or both parents must possess that factor. If both putative parents lack the factor then the offspring is excluded from that parental combination. Factors are identified by a test tube reaction of red cells with a typing reagent appropriately analyzed and identified.

At least 4 of the systems, the A, B, C, and S systems have 2 or more factors inherited as a group = phenogroup. Phenogroups were first disclosed by Dr. Clyde Stormont at the University of Madison, Wisconsin. They were found to parallel the "agglutinogens" concurrently and independently disclosed by Alexander S. Wiener in human agglutination reactions of blood types. Perhaps the most impressive phenogroup is the one coded B2B which has the number one place of highest frequency in Jersey cattle (28%). B2B = B0K0<sub>2</sub>Y<sub>1</sub>A<sub>1</sub>E<sub>1</sub>E<sub>1</sub>'S<sub>1</sub>G<sub>1</sub>'Y<sub>1</sub>O<sub>1</sub>'Y<sub>1</sub>.

DISCUSSION

That events of heterozygote advantage might occur in nature is well known. The day moth, *Panaxia*, with the 3 original "species" *dominula*, *medionigra* and *bimacula* differing by wing spotting patterns were disclosed to be only single gene differences (Ford, 1965). But the pertinence here is that the female *Panaxia* preferred to mate with males of either of the 2 forms different from her. Whether one locus or maximizing heterozygosity at several loci yields the advantage in this case is not demonstrated to my knowledge. The latter assumption seems likely.

Other examples include the white-throated sparrow, *Zonotrichia albicollis*, in which white-throated individuals preferentially choose tan-striped mates (Thornycroft, 1975). A "rare male mating advantage" has been described in several *Drosophila* species and the house fly (Genetics 107: 577). The rare male phenotype presumably is associated with other differing loci, thus assuming an increasing in the progeny as well as a decrease in inbreeding.

There are species in which particular loci are adapted together to fit ecological niches. Some inbreeding is critical and necessary to maintain such groups of genes together. The Japanese quail and Vervet monkeys (Nature 295:236-237/1982 and Science 222:148/1983) are thought to fit this hypothesis. The quail, for example, prefer a first cousin over siblings, third cousins, or unrelated individuals for a mating partner.

Other species can utilize outcrossing by selective advantages of overdominance, heterozygote advantage or whatever related phrases are preferred. Perhaps cattle belong to the latter type. Have mating preferences in cattle ever been studied? Man usually imposes his will on the bulls available to the cows.

Cattle could well utilize H.A. in economic production characters. So why has no one tried? Until blood grouping only a few (often detrimental) characters were known by identified loci. Ten loci plus one more recently (T<sub>1</sub>) in cattle blood groups are well known--some of them with much polymorphism. The B system is the epitome of extreme variation in any species. As stated before over 700 phenogroups are known and this in only a relatively few breeds of cattle. For that reason alone, one could postulate that it is a complex locus, perhaps much more so than the HL-A complex in humans.

The reason for existence of such polymorphism within and among expectations from Rh information, incompatibility of blood type (mother/fetus) is an advantage in rats (Falm, 1974; Beer, 1975). Heterozygote Advantage has been demonstrated in blood groups of humans, and the FV and R.S. heterozygote excess in some cattle (Miller, 1966).

The ten or more genetic systems of blood groups represent perhaps 1/3 of the 60 (30 pairs) chromosomes tagged. New factors could add to this. Adding several electrophoretic characters that exhibit polymorphism in cattle, such as hemoglobin, transferrins, albumin esterase, and carbonic anhydrase could increase this to half of the chromosomes possibly tagged with markers.

Identifying such markers in bulls could lead to better recommendations for herd sires or artificial insemination uses. Selecting for health and type by eye first, then allotting sires by maximum differences in blood types might well increase Heterozygote Advantage.

Possible Applications: Examples

Figure 1 is an example of maximizing the heterozygosity in any offspring of a particular cross in the Nelore breed without driving the parents to homozygosity in all systems. It is unrealistic to the extent that J homozygotes are unlikely from population frequency considerations, and the L homozygotes would be difficult to detect. Otherwise the types are reasonably typical. All progeny for this cross would be heterozygous in all 10 systems in spite of the 256 blood types possible from segregation and assortment.

The number of types possible is the product of the number of types possible in each independent system: e.g. 2 in the A system x 4 in the B system x 4 in the C system x 2 in the M system x 4 in the S system = 256.

Figure 1. Sample Nelore blood type combination to yield maximum Heterozygote Advantage (H.A.).

Male:	A <sub>1</sub> J <sub>1</sub> H	B6X <sub>1</sub> A <sub>1</sub> D <sub>1</sub> E <sub>1</sub> S <sub>1</sub> J <sub>1</sub> O <sub>1</sub> P <sub>1</sub> /B6Q <sub>1</sub> S <sub>1</sub> P <sub>1</sub> Q <sub>1</sub>	C <sub>1</sub> X <sub>1</sub>	V <sub>1</sub> V <sub>1</sub>	J/J	L/L	M/M	SH <sub>1</sub> /UH <sub>1</sub>	Z/Z	R/R
F <sub>1</sub> 's	A <sub>1</sub> J <sub>1</sub> /O	B6X <sub>1</sub> A <sub>1</sub> D <sub>1</sub> E <sub>1</sub> S <sub>1</sub> J <sub>1</sub> O <sub>1</sub> P <sub>1</sub> /P <sub>1</sub> Y <sub>1</sub> A <sub>1</sub>	C <sub>1</sub> /R <sub>1</sub> M <sub>1</sub>	F <sub>1</sub> V <sub>1</sub>	J/-	L/-	M/-	SH <sub>1</sub> /U <sub>1</sub>	Z/-	R <sub>1</sub> /S <sub>1</sub>
D/H	B6X <sub>1</sub> A <sub>1</sub> D <sub>1</sub> E <sub>1</sub> S <sub>1</sub> J <sub>1</sub> O <sub>1</sub> P <sub>1</sub> /T <sub>1</sub> E <sub>1</sub> O <sub>1</sub>	C <sub>1</sub> /E <sub>1</sub>	F <sub>1</sub> V <sub>1</sub>	J/-	L/-	M/-	SH <sub>1</sub> /U <sub>1</sub>	Z/-	R <sub>1</sub> /S <sub>1</sub>	
D/H	B6Q <sub>1</sub> S <sub>1</sub> P <sub>1</sub> Q <sub>1</sub> /P <sub>1</sub> Y <sub>1</sub> A <sub>1</sub>	X <sub>1</sub> /R <sub>1</sub> M <sub>1</sub>	F <sub>1</sub> V <sub>1</sub>	J/-	L/-	M/-	UH <sub>1</sub> /U <sub>1</sub>	Z/-	R <sub>1</sub> /S <sub>1</sub>	
Females:	D/O	P <sub>1</sub> Y <sub>1</sub> A <sub>1</sub> /T <sub>1</sub> E <sub>1</sub> O <sub>1</sub>	R <sub>1</sub> M <sub>1</sub> /E <sub>1</sub>	F <sub>1</sub> F <sub>1</sub>	-/-	-/-	U <sub>1</sub> /U <sub>1</sub>	-/-	S <sub>1</sub> /S <sub>1</sub>	

The middle blood types between male and female parents represent possibilities in each system. The probability of heterozygous offspring = 1 = 100%. There are 256 blood types possible, but all are heterozygotes in 10 systems.

In figure 2 is a sample of the possibility of knowing the maximum of Heterozygote Advantage (HA) for phenogroups in each system. Suppose the interactions of A<sub>1</sub>D<sub>1</sub>Z<sub>1</sub> and H in the A system yielded maximum HA for that system, etcetera for each system in the

hypothetical F<sub>1</sub>. (Some interactions between systems might be anticipated when we actually work on such situations. But for now we can ignore such additional complications). So we can breed and select the homozygosity for the best phenogroups in parental stocks. While only one blood type results, all 10 loci are heterozygous.

Figure 2. Supposition of knowing the maximum H.A. for particular phenogroups and breeding P<sub>1</sub> stocks to yield it.

Male:	A <sub>1</sub> D <sub>1</sub> Z <sub>1</sub> /A <sub>1</sub> D <sub>1</sub> Z <sub>1</sub>	B6X <sub>1</sub> O <sub>1</sub> /B6X <sub>1</sub> O <sub>1</sub>	C <sub>1</sub> R <sub>1</sub> M <sub>1</sub> /C <sub>1</sub> R <sub>1</sub> M <sub>1</sub>	F <sub>1</sub> F <sub>1</sub>	J/J	L/L	M/M	SH <sub>1</sub> /SH <sub>1</sub>	Z/Z	R/R
F <sub>1</sub>	A <sub>1</sub> D <sub>1</sub> Z <sub>1</sub> /H	B6X <sub>1</sub> O <sub>1</sub> /I <sub>1</sub> P <sub>1</sub> E <sub>1</sub> S <sub>1</sub> J <sub>1</sub> O <sub>1</sub> P <sub>1</sub> Q <sub>1</sub>	C <sub>1</sub> R <sub>1</sub> M <sub>1</sub> X <sub>1</sub>	F <sub>1</sub> V <sub>1</sub>	J/-	L/-	M/-	SH <sub>1</sub> /U <sub>1</sub>	Z/-	R <sub>1</sub> /S <sub>1</sub>
Females:	H/H	I <sub>1</sub> P <sub>1</sub> E <sub>1</sub> S <sub>1</sub> J <sub>1</sub> O <sub>1</sub> P <sub>1</sub> Q <sub>1</sub> /I <sub>1</sub> P <sub>1</sub> E <sub>1</sub> S <sub>1</sub> J <sub>1</sub> O <sub>1</sub> P <sub>1</sub> Q <sub>1</sub>	X <sub>1</sub> /X <sub>1</sub>	V <sub>1</sub> V <sub>1</sub>	-/-	-/-	U <sub>1</sub> /U <sub>1</sub>	-/-	S <sub>1</sub> /S <sub>1</sub>	

Why one F<sub>1</sub> blood type; but all 10 loci are heterozygous in the F<sub>1</sub>.

Figure 3 represents the random choice of two reasonably representative Nelore recently tested in our laboratory. If used as parents the F<sub>1</sub> could not be heterozygous in 4 of the systems and only has a 3/128 chance of being heterozygous in as many as 6 systems.

Figure 3. Sample of the current likelihood of H.A. within the Nelore breed. Two random blood types.

Male:	A <sub>1</sub> H/A <sub>1</sub> (H)	B6Q <sub>1</sub> S <sub>1</sub> P <sub>1</sub> Q <sub>1</sub> /B6Q <sub>1</sub> S <sub>1</sub> P <sub>1</sub> Q <sub>1</sub>	C <sub>1</sub> R <sub>1</sub> I <sub>1</sub> L <sub>1</sub>	F <sub>1</sub> F <sub>1</sub>	J/J	L	-/-	UH <sub>1</sub> /U <sub>1</sub>	Z/-	S
F <sub>1</sub>	2	4	2	1	2	(2)	1	(2)	22	1 = 3/256
P	.5	1	.5	0	.5	0	.75	.5	0	= 0.0234
Females:	A <sub>1</sub> D <sub>1</sub> Z <sub>1</sub> /A <sub>1</sub> H	B6I <sub>1</sub> O <sub>1</sub> T <sub>1</sub> /I <sub>1</sub> P <sub>1</sub> E <sub>1</sub> S <sub>1</sub> J <sub>1</sub> O <sub>1</sub> P <sub>1</sub> Q <sub>1</sub>	X <sub>1</sub> /I <sub>1</sub> X <sub>1</sub>	F <sub>1</sub> F <sub>1</sub>	-/-	L	-/-	SH <sub>1</sub> /UH <sub>1</sub>	Z	S

Number of types possible in that system from the indicated parents. Total possible = the product of the number possible in each system. Probability of heterozygosity in 10, 9, or 8, systems = zero; P of heterozygosity in 7 systems = .0.0234

Blood groups, nevertheless, are better than other loci in maximizing heterozygosity in random breeding, since there are very many detected alleles in 2 of the systems and several in 2 other systems. Perhaps "Nature" intended for maximum heterozygosity often in those systems.

The reason for the existence of multiple blood group types has seldom been considered. Miller (1976) notes 4 categories of possible uses "in nature": (1) Physiological consequences including incompatibility (note that with the exception of ABO, Rh and Kell in humans incompatibility is advantageous between mother and fetus); (2) Heterozygote Advantage, per se; (3) Molecular mimicry in which parasites, especially bacteria, find it easy to mask their own antigens against antibody attack by the host in simple antigenic genetic systems; but difficult when the host has controlling multiple alleles present; and (4) Cell membrane function. Heterozygote Advantage could be involved in all of these processes.

BIBLIOGRAPHY

- BEER, G.S. et al. Immunogenetic aspects of implantation, placental and foeto-placental growth rates. Biol.Reprod. 12:176-189, 1975.
- BRILES, W.E. Current status of blood groups in domestic birds. Z.Tierzücht.ZüchtBiol. 79:371-391, 1964.
- CONNELLY, F.M. & STONE, W.H. Association between a blood group and butter fat production in dairy cattle. Nature, 206-115, 1965.
- MILLER, W.J. Blood groups in Longhorn cattle. Genetics 54:391-404, 1966.
- NEIMANN-SØRENSEN, A. & ROBERTSON, A. The association between blood groups and several production characteristics in three Danish cattle breeds. Acta Agric.Scand. 11:163-196, 1961.
- FENEDO, M.C.T. Análise de polimorfismos imunogenéticos e bioquímicos em gado Holandês, Guzerá e seus mestiços. Tese de mestrado. Fac.Med. USP, Rib.Preto, 1981.
- RENDEL, J. Recent studies on relationships between blood groups and production characters in farm animals. Z.Tierzücht.ZüchtBiol. 75:97-109, 1961.